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* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1          Web Page for STN Seminar Schedule - N. America
 NEWS  2  NOV 21  CAS patent coverage to include exemplified prophetic
                  substances identified in English-, French-, German-,
                  and Japanese-language basic patents from 2004-present
 NEWS  3  NOV 26  MARPAT enhanced with FSORT command
 NEWS  4  NOV 26  CHEMSAFE now available on STN Easy
 NEWS  5  NOV 26  Two new SET commands increase convenience of STN
                  searching
 NEWS  6  DEC 01  ChemPort single article sales feature unavailable
 NEWS  7  DEC 12  GBFULL now offers single source for full-text
                  coverage of complete UK patent families
 NEWS  8  DEC 17  Fifty-one pharmaceutical ingredients added to PS
 NEWS  9  JAN 06  The retention policy for unread STNmail messages
                  will change in 2009 for STN-Columbus and STN-Tokyo
 NEWS 10  JAN 07  WPIDS, WPINDEX, and WPIX enhanced Japanese Patent
                  Classification Data

 NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
              AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS LOGIN    Welcome Banner and News Items
 NEWS IPC8     For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that
specific topic.

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* * * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 23:44:57 ON 01 FEB 2009

=> index bioscience medicine
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.22       0.22

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
       AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
       CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
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       DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 23:45:17 ON 01 FEB 2009

71 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s t7 (3a)(endo or endonucleas?)(3a)(1 or i)
          2   FILE AGRICOLA
          5   FILE BIOENG
         62   FILE BIOSIS
         18   FILE BIOTECHABS
         18   FILE BIOTECHDS
         27   FILE BIOTECHNO
  13 FILES SEARCHED...
         88   FILE CAPLUS
         59   FILE DGENE
          2   FILE DISSABS
          1   FILE DRUGU
  27 FILES SEARCHED...
         50   FILE EMBASE
         38   FILE ESBIOBASE
         57   FILE GENBANK
  35 FILES SEARCHED...
         34   FILE IFIPAT
         40   FILE LIFESCI
         56   FILE MEDLINE
         12   FILE PASCAL
  51 FILES SEARCHED...
         66   FILE SCISEARCH
         21   FILE TOXCENTER
         25   FILE USGENE
        103   FILE USPATFULL
  61 FILES SEARCHED...
         14   FILE USPAT2
         25   FILE WPIDS
         25   FILE WPINDEX

  24 FILES HAVE ONE OR MORE ANSWERS,   71 FILES SEARCHED IN STNINDEX

L1   QUE T7 (3A)(ENDO OR ENDONUCLEAS?)(3A)(1 OR I)

=> d rank
F1         103   USPATFULL
F2          88   CAPLUS
F3          66   SCISEARCH
F4          62   BIOSIS
F5          59   DGENE
F6          57   GENBANK
F7          56   MEDLINE
F8          50   EMBASE
F9          40   LIFESCI
F10         38   ESBIOBASE
F11         34   IFIPAT
F12         27   BIOTECHNO
F13         25   USGENE
F14         25   WPIDS
F15         25   WPINDEX
F16         21   TOXCENTER
F17         18   BIOTECHABS
F18         18   BIOTECHDS
F19         14   USPAT2
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F20          12   PASCAL
F21           5   BIOENG
F22           2   AGRICOLA
F23           2   DISSABS
F24           1   DRUGU


=> file f1-f4, f7-15
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       4.08       4.30

FILE 'USPATFULL' ENTERED AT 23:48:56 ON 01 FEB 2009
CA INDEXING COPYRIGHT (C) 2009 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'CAPLUS' ENTERED AT 23:48:56 ON 01 FEB 2009
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FILE 'WPIDS' ENTERED AT 23:48:56 ON 01 FEB 2009
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FILE 'WPINDEX' ACCESS NOT AUTHORIZED

=> s t7 (3a)(endo or endonucleas?)(3a)(1 or i)
   8 FILES SEARCHED...
L2          614 T7 (3A)(ENDO OR ENDONUCLEAS?)(3A)(1 OR I)

=> s l2(s)(modif? or muta? or delet? or inser?)
  11 FILES SEARCHED...
L3          203 L2(S)(MODIF? OR MUTA? OR DELET? OR INSER?)

=> s l3 and beta?
L4           89 L3 AND BETA?
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=> dup rem l4
DUPLICATE IS NOT AVAILABLE IN 'USGENE'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L4
L5           74 DUP REM L4 (15 DUPLICATES REMOVED)

=> d ti l5 1-74

L5   ANSWER 1 OF 74  USPATFULL on STN
TI     DETECTION OF TARGET MOLECULES THROUGH INTERACTION WITH PROBES

L5   ANSWER 2 OF 74  USPATFULL on STN
TI     Cell Free Biosynthesis of High-Quality Nucleic Acid and Uses Thereof

L5   ANSWER 3 OF 74  USPATFULL on STN
TI     Methods and Compositions for Assessment of Pulmonary Function and
       Disorders

L5   ANSWER 4 OF 74  USPATFULL on STN
TI     Enrichment Through Heteroduplexed Molecules

L5   ANSWER 5 OF 74  USPATFULL on STN
TI     Single molecule arrays for genetic and chemical analysis

L5   ANSWER 6 OF 74  USPATFULL on STN
TI     Methods of Analysis of Polymorphisms and Uses Thereof

L5   ANSWER 7 OF 74  USPATFULL on STN
TI     Selective cloning of homoduplex nucleic acids

L5   ANSWER 8 OF 74  CAPLUS  COPYRIGHT 2009 ACS on STN DUPLICATE 1
TI   The structure of a fibril-forming sequence, NNQQNY, in the context of a
     globular fold

L5   ANSWER 9 OF 74  USPATFULL on STN                    DUPLICATE 2
TI     Modified dna cleavage enzymes and methods for use (as amended by isa)

L5   ANSWER 10 OF 74  USPATFULL on STN
TI     Methods for assembly of high fidelity synthetic polynucleotides

L5   ANSWER 11 OF 74  USPATFULL on STN
TI     Methods for assembly of high fidelity synthetic polynucleotides

L5   ANSWER 12 OF 74  USPATFULL on STN
TI     Single molecule arrays for genetic and chemical analysis

L5   ANSWER 13 OF 74  USPATFULL on STN
TI     Methods and compositions for assessment of pulmonary function and
       disorders

L5   ANSWER 14 OF 74  USPATFULL on STN
TI     Array oligomer synthesis and use

L5   ANSWER 15 OF 74  USPATFULL on STN
TI     Making nucleic acid sequences in parallel and use

L5   ANSWER 16 OF 74  USPATFULL on STN
TI     Mobility-Modified Nucleobase Polymers and Methods of Using Same

L5   ANSWER 17 OF 74  WPIDS COPYRIGHT 2009       THOMSON REUTERS on STN
TI   Repairing a damaged polynucleotide to enhance fidelity or yield of its
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copied or amplified product by incubating the polynucleotide in a reaction mixture comprising and enhancing fidelity or yield of the copied or amplified product

L5 ANSWER 18 OF 74 LIFESCI COPYRIGHT 2009 CSA on STN DUPLICATE 3
TI The Mechanism of the Amyloidogenic Conversion of T7 Endonuclease I

L5 ANSWER 19 OF 74 USPATFULL on STN DUPLICATE 4
TI Repair of nucleic acids for improved amplification

L5 ANSWER 20 OF 74 USPATFULL on STN
TI Methods and compositions for assessment of pulmonary function and disorders

L5 ANSWER 21 OF 74 USPATFULL on STN
TI Methods of analysis of polymorphisms and uses thereof

L5 ANSWER 22 OF 74 USPATFULL on STN
TI Methods and compositions for assessment of pulmonary function and disorders

L5 ANSWER 23 OF 74 USPATFULL on STN
TI Methods for assembly of high fidelity synthetic polynucleotides

L5 ANSWER 24 OF 74 USPATFULL on STN
TI Populations of reporter sequences and methods of their use

L5 ANSWER 25 OF 74 USPATFULL on STN
TI Error reduction in automated gene synthesis

L5 ANSWER 26 OF 74 USPATFULL on STN
TI Polynucleotide synthesis

L5 ANSWER 27 OF 74 USPATFULL on STN
TI Preparation of defined highly labeled probes

L5 ANSWER 28 OF 74 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 5
TI Alteration of DNA cleaving enzyme activity by changing reciprocal stereo-geometric positions of two catalytic centers, and use of the enzyme for the identification of an SNP

L5 ANSWER 29 OF 74 USPATFULL on STN
TI Selective cloning of homoduplex nucleic acids

L5 ANSWER 30 OF 74 USPATFULL on STN
TI Methods and compositions for whole genome amplification and genotyping

L5 ANSWER 31 OF 74 USPATFULL on STN
TI Charge and mass tags for detection and analysis

L5 ANSWER 32 OF 74 USPATFULL on STN
TI Methods and compositions for whole genome amplification and genotyping

L5 ANSWER 33 OF 74 USPATFULL on STN
TI Methods and compositions for whole genome amplification and genotyping

L5 ANSWER 34 OF 74 USPATFULL on STN
TI Mobility-modified nucleobase polymers and methods of using same

L5 ANSWER 35 OF 74 USPATFULL on STN
TI Methods and compositions for whole genome amplification and genotyping

L5 ANSWER 36 OF 74 USPATFULL on STN
TI Detection of target molecules through interaction with probes

L5 ANSWER 37 OF 74 USPATFULL on STN
TI Synthetic peptides and uses therefore

L5 ANSWER 38 OF 74 USPATFULL on STN
TI Selective cloning of homoduplex nucleic acids

L5 ANSWER 39 OF 74 USPATFULL on STN
TI Endonuclease VII cloning method

L5 ANSWER 40 OF 74 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 6
TI Changing the enzymatic activity of T7 endonuclease by mutations at the beta-bridge site: Alteration of substrate specificity profile and metal ion requirements by mutation distant from the catalytic domain.

L5 ANSWER 41 OF 74 USPATFULL on STN
TI Maxam gilbert g/a sequence analysis by DHPLC

L5 ANSWER 42 OF 74 USPATFULL on STN
TI Mobility-modified nucleobase polymers and methods of using same

L5 ANSWER 43 OF 74 USPATFULL on STN
TI Method for DNA footprinting

L5 ANSWER 44 OF 74 USPATFULL on STN
TI Fixed address analysis of sequence tags

L5 ANSWER 45 OF 74 USPATFULL on STN
TI Method for detecting and identifying mutations

L5 ANSWER 46 OF 74 USPATFULL on STN
TI Fixed address analysis of sequence tags

L5 ANSWER 47 OF 74 LIFESCI COPYRIGHT 2009 CSA on STN DUPLICATE 7
TI Evaluation of PCR-generated chimeras, mutations, and heteroduplexes with 16S rRNA gene-based cloning

L5 ANSWER 48 OF 74 USPATFULL on STN
TI Detection of mutation by resolvase cleavage

L5 ANSWER 49 OF 74 USPATFULL on STN
TI Detection of mutation by resolvase cleavage

L5 ANSWER 50 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 51 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 52 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 53 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 54 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 55 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 56 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 57 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 58 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 59 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 60 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 61 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 62 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 63 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 64 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 65 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 66 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 67 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 68 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa) (PublishedApplication)

L5 ANSWER 69 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)

(PublishedApplication)

L5 ANSWER 70 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 71 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 72 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 73 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

L5 ANSWER 74 OF 74 USGENE COPYRIGHT 2009 SEQUENCEBASE CORP on STN
TI Modified dna cleavage enzymes and methods for use (as amended by isa)
(PublishedApplication)

=> d ibib abs 15 8-10 17 28 32 39-40

L5 ANSWER 8 OF 74 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2008:1098323 CAPLUS
DOCUMENT NUMBER: 149:507387
TITLE: The structure of a fibril-forming sequence, NNQQNY, in the context of a globular fold
AUTHOR(S): Guo, Zhefeng; Eisenberg, David
CORPORATE SOURCE: Howard Hughes Medical Institute, UCLA-DOE Institute for Genomics and Proteomics, Molecular Biology Institute, UCLA, Los Angeles, CA, 90095-1570, USA
SOURCE: Protein Science (2008), 17(9), 1617-1623
CODEN: PRCIEI; ISSN: 0961-8368
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Numerous human disorders are associated with the formation of protein fibrils. The fibril-forming capacity of a protein has been found in recent studies to be determined by a short segment of residues that forms a dual β -sheet, called a steric zipper, in the spine of the fibril. The question arises as to whether a fibril-forming segment, when inserted within the sequence of a globular protein, will invariably cause the protein to form fibrils. Here we investigate this question by inserting the known fibril-forming segment NNQQNY into the globular enzyme, T7 endonuclease I. From earlier studies, we know that in its fibril form, NNQQNY is in an extended conformation. We first found that the inserted NNQQNY stimulates fibril formation of T7 endonuclease I in solution Thus NNQQNY within T7 endonuclease I can exist in an extended conformation, capable of forming the steric zipper in the core of a fibril. We also found that T7 endonuclease I folds into a decamer that does not form fibrils. We determined the structure of the decamer by X-ray crystallog., finding an unusual oligomer without point group symmetry, and finding that the NNQQNY segments within the decamer adopt two twisted conformations, neither is apparently able to fibrillize. We conclude that twisting of fibril forming sequences from the fully extended conformation, imposed by the context of their placement in proteins, can interfere with fibril formation.
REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 9 OF 74 USPATFULL on STN DUPLICATE 2
ACCESSION NUMBER: 2007:48556 USPATFULL
TITLE: Modified dna cleavage enzymes and methods for use (as amended by isa)
INVENTOR(S): Guan, Chudi, Wenham, MA, UNITED STATES
Kumar, Sanjay, Ipswitch, MA, UNITED STATES
Kucera, Rebecca, Hamilton, MA, UNITED STATES
PATENT ASSIGNEE(S): New England Biolabs, Inc., Ipswich, MA, UNITED STATES, 01938 (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 20070042379	A1	20070222	
APPLICATION INFO.:	US 2004-585964	A1	20041122	(10)
	WO 2004-US39288		20041122	
			20060713	PCT 371 date

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: HARRIET M. STRIMPEL, NEW ENGLAND BIOLABS, INC., 240 COUNTY ROAD, IPSWICH, MA, 01938-2723, US
NUMBER OF CLAIMS: 31
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 22 Drawing Page(s)
LINE COUNT: 1360
AB Compositions and methods are provided that relate to a modified DNA cleaving enzyme having at least 35% amino acid sequence identity with T7 Endo I. The modified enzyme includes two catalytic centers separated by a .beta .-bridge where the β -bridge contains at least one mutation having an effect of altering enzyme cleavage activity compared to the unmodified enzyme. Activities associated with the modified DNA cleaving enzyme that can be modulated in different reaction conditions include at least one of: (a) non-sequence specific nicking activity; (b) cleaving the second strand of a duplex DNA at a preexisting nick site to produce a linear duplex with a single strand overhang; (c) non-sequence specific DNA cleavage; (d) cleaving DNA flanking a mismatch; and (e) cleavage at a cruciform structure in a DNA duplex.

L5 ANSWER 10 OF 74 USPATFULL on STN
ACCESSION NUMBER: 2007:308772 USPATFULL
TITLE: Methods for assembly of high fidelity synthetic polynucleotides
INVENTOR(S): Church, George, Brookline, MA, UNITED STATES
Afeyan, Noubar, Lexington, MA, UNITED STATES
Jacobson, Joseph, Newton, MA, UNITED STATES
Baynes, Brian M., Somerville, MA, UNITED STATES
Nesmith, Kenneth Gabriel, Cambridge, MA, UNITED STATES
Chapman, Brad Alan, Somerville, MA, UNITED STATES
Strack-Logue, Bettina, Somerville, MA, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 20070269870	A1	20071122	
APPLICATION INFO.:	US 2005-254250	A1	20051018	(11)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2005-68321, filed on 28 Feb 2005, PENDING Continuation-in-part of Ser. No. US 2005-67812, filed on 28 Feb 2005, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 2004-619650P	20041018 (60)
	US 2005-657014P	20050228 (60)
	US 2005-698560P	20050712 (60)
	US 2005-643813P	20050113 (60)
	US 2005-727205P	20051014 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: ROPES & GRAY LLP, PATENT DOCKETING 39/41, ONE INTERNATIONAL PLACE, BOSTON, MA, 02110-2624, US
NUMBER OF CLAIMS: 21
EXEMPLARY CLAIM: 1-291
NUMBER OF DRAWINGS: 36 Drawing Page(s)
LINE COUNT: 5051
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Disclosed are methods of manufacturing synthetic DNAs, that is, DNAs made at least in significant part by chemical synthesis of nucleic acid polymers. Also provided are methods for assembling plural DNAs in the same pool by multiplexed assembly of synthetic oligonucleotides. In exemplary embodiments, the methods involve pre-amplification of one or more oligonucleotides using "universal" primers, reduction of the error rate in oligonucleotide and/or nucleic acid products, and sequence optimization and oligonucleotides design. Also provided are low-purity arrays of nucleic acids and methods for assembling nucleic acids using oligonucleotides obtained from low-purity arrays.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 74 WPIDS COPYRIGHT 2009 THOMSON REUTERS on STN
ACCESSION NUMBER: 2007-805625 [75] WPIDS
DOC. NO. CPI: C2007-279817 [75]
TITLE: Repairing a damaged polynucleotide to enhance fidelity or yield of its copied or amplified product by incubating the polynucleotide in a reaction mixture comprising and enhancing fidelity or yield of the copied or amplified product
DERWENT CLASS: B04; D16
INVENTOR: CHEN L; EVANS T C; GUAN C; KUCERA R; SLATKO B; VAISVILA R; EVANS T
PATENT ASSIGNEE: (NEWE-C) NEW ENGLAND BIOLABS INC
COUNTRY COUNT: 119

PATENT INFO ABBR.:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2007120627	A2	20071025	(200775)*	EN	137[20]	
WO 2007120627	A3	20071227	(200803)	EN		
EP 2010678	A2	20090107	(200906)	EN		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2007120627	A2	WO 2007-US8792	20070411
EP 2010678	A2	EP 2007-755155	20070411
EP 2010678	A2 PCT Application	WO 2007-US8792	20070411

FILING DETAILS:

PATENT NO	KIND	PATENT NO

EP 2010678 A2 Based on WO 2007120627 A

PRIORITY APPLN. INFO: US 2006-791056P 20060411
AN 2007-805625 [75] WPIDS
AB WO 2007120627 A2 UPAB: 20090130
NOVELTY - Repairing a damaged polynucleotide so as to enhance at least one of fidelity and yield of a copied or amplified product of the polynucleotide comprises incubating the polynucleotide in a reaction mixture comprising apurinic/apyrimidinic (AP) endonuclease; a DNA ligase; and NAD or ATP as a cofactor; and enhancing fidelity or yield of the copied or amplified product.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are:
(1) a kit;
(2) a polynucleotide repair mixture;
(3) a method for cloning or sequencing a polynucleotide fragment;
(4) a method for enhancing the yield of a copied or amplified polynucleotide;
(5) a method for sequencing a polynucleotide; and
(6) a method for copying or amplifying a fragmented DNA.
USE - The method is useful in repairing a damaged polynucleotide so as to enhance fidelity or yield of a copied or amplified product of the polynucleotide (claimed).

L5 ANSWER 28 OF 74 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 5
ACCESSION NUMBER: 2005:490414 CAPLUS
DOCUMENT NUMBER: 143:40003
TITLE: Alteration of DNA cleaving enzyme activity by changing reciprocal stereo-geometric positions of two catalytic centers, and use of the enzyme for the identification of an SNP
INVENTOR(S): Guan, Chudi; Kumar, Sanjay; Kucera, Rebecca
PATENT ASSIGNEE(S): New England Biolabs, Inc., USA
SOURCE: PCT Int. Appl., 80 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005052124	A2	20050609	WO 2004-US39288	20041122
WO 2005052124	A3	20051027		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
EP 1702063	A2	20060920	EP 2004-811921	20041122
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, FI, RO, CY, TR, BG, CZ, EE, HU, PL, SK, IS				
CN 1906292	A	20070131	CN 2004-80040697	20041122
IN 2006DN03516	A	20070831	IN 2006-DN3516	20060619
US 20070042379	A1	20070222	US 2006-585964	20060713
PRIORITY APPLN. INFO.:			US 2003-524123P P	20031121

WO 2004-US39288 W 20041122

AB Compns. and methods are provided that relate to a modified DNA cleaving enzyme having at least 35% amino acid sequence identity with T7 endonuclease I (T7 Endo I). The modified enzyme includes two catalytic centers separated by a β -bridge where the β -bridge contains at least one mutation having an effect of altering enzyme cleavage activity compared to the unmodified enzyme. Activities associated with the modified DNA cleaving enzyme that can be modulated in different reaction conditions include at least one of: (a) non-sequence specific nicking activity; (b) cleaving the second strand of a duplex DNA at a preexisting nick site to produce a linear duplex with a single strand overhang; (c) non-sequence specific DNA cleavage; (d) cleaving DNA flanking a mismatch; and (e) cleavage at a cruciform structure in a DNA duplex. The modified DNA cleaving enzyme can be used for the identification of the location of an SNP. A feature of the modified T7 Endo I is reduced toxicity in a host cell permitting overexpression of the DNA cleaving enzyme.

L5 ANSWER 32 OF 74 USPATFULL on STN
ACCESSION NUMBER: 2005:68909 USPATFULL
TITLE: Methods and compositions for whole genome amplification and genotyping
INVENTOR(S): Gunderson, Kevin, Encinitas, CA, UNITED STATES
Steemers, Frank, San Diego, CA, UNITED STATES
PATENT ASSIGNEE(S): Illumina, Inc., San Diego, CA (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 20050059048	A1	20050317
APPLICATION INFO.:	US 2004-872141	A1	20040617 (10)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2003-681800, filed on 8 Oct 2003, PENDING Continuation of Ser. No. US 2003-600634, filed on 20 Jun 2003, PENDING
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: John T. Murphy, Illumina, Inc., 9885 Towne Centre Drive, San Diego, CA, 92121-1975
NUMBER OF CLAIMS: 52
EXEMPLARY CLAIM: CLM-01-77
NUMBER OF DRAWINGS: 18 Drawing Page(s)
LINE COUNT: 5277
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides methods of amplifying genomic DNA to obtain an amplified representative population of genome fragments. Methods are further provided for obtaining amplified genomic DNA representations of a desired complexity. The invention further provides methods for simultaneously detecting large numbers of typable loci for an amplified representative population of genome fragments. Accordingly the methods can be used to genotype individuals on a genome-wide scale.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 39 OF 74 USPATFULL on STN
ACCESSION NUMBER: 2004:2134 USPATFULL
TITLE: Endonuclease VII cloning method
INVENTOR(S): Greener, Alan L., San Diego, CA, UNITED STATES
Hexdall, Lisa Joy, San Diego, CA, UNITED STATES
Carstens, Carsten-Peter, San Diego, CA, UNITED STATES
Sorge, Joseph A., Wilson, WY, UNITED STATES
PATENT ASSIGNEE(S): Stratagene (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 20040002155	A1	20040101
APPLICATION INFO.:	US 2002-180174	A1	20020626 (10)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: PALMER & DODGE, LLP, KATHLEEN M. WILLIAMS / STR, 111 HUNTINGTON AVENUE, BOSTON, MA, 02199
NUMBER OF CLAIMS: 38
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 4 Drawing Page(s)
LINE COUNT: 1111
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The subject invention provides for a strain of host cells that contains a temperature sensitive variant of the gene encoding the endonuclease VII from phage T4. Using this host strain, the invention features a novel cloning method that selects for PCR products that are devoid of PCR-generated mutations.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 40 OF 74 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 6

ACCESSION NUMBER: 2004:267671 BIOSIS
DOCUMENT NUMBER: PREV200400268291
TITLE: Changing the enzymatic activity of T7 endonuclease by mutations at the beta-bridge site: Alteration of substrate specificity profile and metal ion requirements by mutation distant from the catalytic domain.
AUTHOR(S): Guan, Chudi [Reprint Author]; Kumar, Sanjay; Kucera, Rebecca; Ewel, Amy
CORPORATE SOURCE: New England Biolabs Inc, 32 Tozer Rd, Beverly, MA, 01915, USA
Guan@neb.com
SOURCE: Biochemistry, (April 13 2004) Vol. 43, No. 14, pp. 4313-4322. print.
ISSN: 0006-2960 (ISSN print).
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 26 May 2004
Last Updated on STN: 26 May 2004

AB Phage-encoded resolvase T7 endonuclease I is a structure-specific endonuclease. The enzyme acts on a broad spectrum of substrates with a variety of DNA structures. The enzyme is a dimer with two separated catalytic domains connected by an elongated beta-sheet bridge. The activities of enzymes with mutations in the beta-bridge segment were studied. Mutations that did not affect catalytic domain folding and function but did alter the relative positions of these domains retained catalytic activity but with altered specificity and metal ion dependence. Our results suggest that the enzyme recognizes its substrates by DNA conformation exclusion and offer a simple explanation for the broad substrate specificity of phage resolvase.

=> d his full

(FILE 'HOME' ENTERED AT 23:44:57 ON 01 FEB 2009)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 23:45:17 ON 01 FEB 2009

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               5   FILE BIOENG
              62   FILE BIOSIS
              18   FILE BIOTECHABS
              18   FILE BIOTECHDS
              27   FILE BIOTECHNO
              88   FILE CAPLUS
              59   FILE DGENE
               2   FILE DISSABS
               1   FILE DRUGU
              50   FILE EMBASE
              38   FILE ESBIOBASE
              57   FILE GENBANK
              34   FILE IFIPAT
              40   FILE LIFESCI
              56   FILE MEDLINE
              12   FILE PASCAL
              66   FILE SCISEARCH
              21   FILE TOXCENTER
              25   FILE USGENE
             103   FILE USPATFULL
              14   FILE USPAT2
              25   FILE WPIDS
              25   FILE WPINDEX
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L3           203 SEA L2(S)(MODIF? OR MUTA? OR DELET? OR INSER?)
L4            89 SEA L3 AND BETA?
L5            74 DUP REM L4 (15 DUPLICATES REMOVED)
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                 D IBIB ABS L5 8-10 17 28 32 39-40


     FILE HOME

     FILE STNINDEX

     FILE USPATFULL
     FILE COVERS 1971 TO PATENT PUBLICATION DATE: 29 Jan 2009 (20090129/PD)
     FILE LAST UPDATED: 29 Jan 2009 (20090129/ED)
     HIGHEST GRANTED PATENT NUMBER: US7484247
     HIGHEST APPLICATION PUBLICATION NUMBER: US20090031463
     CA INDEXING IS CURRENT THROUGH 29 Jan 2009 (20090129/UPCA)
     ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 29 Jan 2009 (20090129/PD)
     REVISED CLASS FIELDS (/NCL) LAST RELOADED: Dec 2008
     USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Dec 2008

     USPATFULL now includes complete International Patent Classification (IPC)
     reclassification data for the third quarter of 2008.

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